

# SEQUENCE LISTING

<110> Kennedy, Giulia  
Kang, Sanmao  
Reinhard, Christoph  
Jefferson, Anne Bennett

<120> POLYNUCLEOTIDES RELATED TO COLON CANCER

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<140> Unassigned

<141> 2001-06-14

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<151> 2000-06-15

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1				5					10	

cat gtg cgg ggg gtg ggg tcc cgt ggc ttc ccc ctg cgc ctc cag gcc  
101

His	Val	Arg	Gly	Val	Gly	Ser	Arg	Gly	Phe	Pro	Leu	Arg	Leu	Gln	Ala
			15					20						25	

acc gag gtc cgt atc tgc cct gtg gaa ttc aac ccc aac ttc gtg gcg  
149

Thr	Glu	Val	Arg	Ile	Cys	Pro	Val	Glu	Phe	Asn	Pro	Asn	Phe	Val	Ala
		30					35					40			

cgt atg ata cct aaa gtg gag tgg tcg gcg ttc ctg gag gcg gcc gat  
197

Arg	Met	Ile	Pro	Lys	Val	Glu	Trp	Ser	Ala	Phe	Leu	Glu	Ala	Ala	Asp
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245

Asn	Leu	Arg	Leu	Ile	Gln	Val	Pro	Lys	Gly	Pro	Val	Glu	Gly	Tyr	Glu
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gag aat gag gag ttt ctg agg acc atg cac cac ctg ctg ctg gag gtg  
293

Glu Asn Glu Glu Phe Leu Arg Thr Met His His Leu Leu Leu Glu Val  
80 85 90

gaa gtg ata gag ggc acc ctg cag tgc ccg gaa tct gga cgt atg ttc  
341

Glu Val Ile Glu Gly Thr Leu Gln Cys Pro Glu Ser Gly Arg Met Phe  
95 100 105

ccc atc agc cgc ggg atc ccc aac atg ctg ctg agt gaa gag gaa act  
389

Pro Ile Ser Arg Gly Ile Pro Asn Met Leu Leu Ser Glu Glu Glu Thr  
110 115 120

gag agt t gattgtgcca ggcgccagtt tttcttgta tgactgtgta tttttgtga  
446

Glu Ser  
125

tctataccct gtttcgaat tctgccgtgt gtatcccaa cccttgaccc aatgacacca  
506

aacacagtgt ttttgagctc ggtattatat atttttttct cattaaaggt ttaaaacc  
564

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Cys Pro Val Glu Phe Asn Pro Asn Phe Val Ala Arg Met Ile Pro Lys  
35 40 45

Val Glu Trp Ser Ala Phe Leu Glu Ala Ala Asp Asn Leu Arg Leu Ile  
50 55 60

Gln Val Pro Lys Gly Pro Val Glu Gly Tyr Glu Glu Asn Glu Glu Phe  
65 70 75 80

Leu Arg Thr Met His His Leu Leu Leu Glu Val Glu Val Ile Glu Gly  
85 90 95

Thr Leu Gln Cys Pro Glu Ser Gly Arg Met Phe Pro Ile Ser Arg Gly  
100 105 110

Ile Pro Asn Met Leu Leu Ser Glu Glu Glu Thr Glu Ser  
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 cacttccaag gactcttgct atctgcctta ggccgggaa atg ctg ttg ctg gat tgc  
 236

Met Leu Leu Leu Asp Cys  
 1 5

aac ccc gag gtg gat ggt ctg aag cat ttg ctg gag aca ggg gcc tcg  
 284

Asn Pro Glu Val Asp Gly Leu Lys His Leu Leu Glu Thr Gly Ala Ser  
 10 15 20

gtc aac gca ccc ccg gat ccc tgc aag cag tcg cct gtc cac tta gcc  
 332

Val Asn Ala Pro Pro Asp Pro Cys Lys Gln Ser Pro Val His Leu Ala  
 25 30 35

gca gga agc ggc ctt gct tgc ttt ctt ctc tgg cag ctg caa acg ggc  
 380

Ala Gly Ser Gly Leu Ala Cys Phe Leu Leu Trp Gln Leu Gln Thr Gly  
 40 45 50

gct gac ctc aac cag cag gat gtt tta gga gaa gct cca cta cac aag  
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Ala Asp Leu Asn Gln Gln Asp Val Leu Gly Glu Ala Pro Leu His Lys  
 55 60 65 70

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Ala Ala Lys Val Gly Ser Leu Glu Cys Leu Ser Leu Leu Val Ala Ser  
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 524

Asp Ala Gln Ile Asp Leu Cys Asn Lys Asn Gly Gln Thr Ala Glu Asp  
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 572

Leu Ala Trp Ser Cys Gly Phe Pro Asp Cys Ala Lys Phe Leu Thr Thr  
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att aaa tgt atg cag aca ata aaa gca agt gaa cac cct gac agg aat  
 620

Ile Lys Cys Met Gln Thr Ile Lys Ala Ser Glu His Pro Asp Arg Asn  
 120 125 130

gat tgt gtt gcc gtg ctc aga cag aaa cgg agt ctc gga agt gta gaa  
 668

Asp Cys Val Ala Val Leu Arg Gln Lys Arg Ser Leu Gly Ser Val Glu  
 135 140 145 150

aat acc agt ggg aaa agg aag tgc t gatgtcacgt gggttatgaa

713

Asn Thr Ser Gly Lys Arg Lys Cys

155

gaagtctgaa gaacgccttc atttcatgca aatctataag ctctctgcttt tggctttacc

773

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<213> H. sapiens

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Ser Pro Val His Leu Ala Ala Gly Ser Gly Leu Ala Cys Phe Leu Leu

35

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45

Trp Gln Leu Gln Thr Gly Ala Asp Leu Asn Gln Gln Asp Val Leu Gly

50

55

60

Glu Ala Pro Leu His Lys Ala Ala Lys Val Gly Ser Leu Glu Cys Leu

65

70

75

80

Ser Leu Leu Val Ala Ser Asp Ala Gln Ile Asp Leu Cys Asn Lys Asn

85

90

95

Gly Gln Thr Ala Glu Asp Leu Ala Trp Ser Cys Gly Phe Pro Asp Cys

100

105

110

Ala Lys Phe Leu Thr Thr Ile Lys Cys Met Gln Thr Ile Lys Ala Ser

115

120

125

Glu His Pro Asp Arg Asn Asp Cys Val Ala Val Leu Arg Gln Lys Arg

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140

Ser Leu Gly Ser Val Glu Asn Thr Ser Gly Lys Arg Lys Cys

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15

ctg tac atg gtg aat gga cca cca cat ttt aca gaa agc aca gtg ttt

97

Leu Tyr Met Val Asn Gly Pro Pro His Phe Thr Glu Ser Thr Val Phe  
20 25 30

cca agg gaa tct ggg aag aat tgc aaa gtc tgt atc ttt agt aag gat  
145  
Pro Arg Glu Ser Gly Lys Asn Cys Lys Val Cys Ile Phe Ser Lys Asp  
35 40 45

ggg acc ttg ttt gcc tgg ggc aat gga gaa aaa gta aat att atc agt  
193  
Gly Thr Leu Phe Ala Trp Gly Asn Gly Glu Lys Val Asn Ile Ile Ser  
50 55 60

gtc act aac aag gga cta ctg cac tcc ttc gac ctc ctg aag gca gtt  
241  
Val Thr Asn Lys Gly Leu Leu His Ser Phe Asp Leu Leu Lys Ala Val  
65 70 75

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289  
Cys Leu Glu Phe Ser Pro Lys Asn Thr Val Leu Ala Thr Trp Gln Pro  
80 85 90 95

tac act act tct aaa gat ggc aca gct ggg ata ccc aac cta caa ctt  
337  
Tyr Thr Thr Ser Lys Asp Gly Thr Ala Gly Ile Pro Asn Leu Gln Leu  
100 105 110

tat gat gtg aaa act ggg aca tgt ttg aaa tct ttc atc cag aaa aaa  
385  
Tyr Asp Val Lys Thr Gly Thr Cys Leu Lys Ser Phe Ile Gln Lys Lys  
115 120 125

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433  
Met Gln Asn Trp Cys Pro Ser Trp Ser Glu Asp Glu Thr Leu Cys Ala  
130 135 140

cgc aat gtt aac aat gaa gtt cac ttc ttt gaa aac aac aat ttt aac  
481  
Arg Asn Val Asn Asn Glu Val His Phe Phe Glu Asn Asn Asn Phe Asn  
145 150 155

aca att gca aat aaa ttg cat ttg caa aaa att aat gac ttt gta tta  
529  
Thr Ile Ala Asn Lys Leu His Leu Gln Lys Ile Asn Asp Phe Val Leu  
160 165 170 175

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577  
Ser Pro Gly Pro Gln Pro Tyr Lys Val Ala Val Tyr Val Pro Gly Ser  
180 185 190

aaa ggt gca cct tca ttt gtt aga tta tat cag tac ccc aac ttt gct  
625  
Lys Gly Ala Pro Ser Phe Val Arg Leu Tyr Gln Tyr Pro Asn Phe Ala  
195 200 205

gga cct cat gca gct tta gct aat aaa agt ttc ttt aag gca gat aaa  
673

Gly Pro His Ala Ala Leu Ala Asn Lys Ser Phe Phe Lys Ala Asp Lys  
210 215 220

gtt aca atg ctg tgg aat aaa aaa gct act gct gtg ttg gta ata gct  
721

Val Thr Met Leu Trp Asn Lys Lys Ala Thr Ala Val Leu Val Ile Ala  
225 230 235

agc aca gat gtt gac aag aca gga gct tcc tac tat gga gaa caa act  
769

Ser Thr Asp Val Asp Lys Thr Gly Ala Ser Tyr Tyr Gly Glu Gln Thr  
240 245 250 255

cta cac tac att gca aca aat gga gaa agt gct gta gtg caa tta cca  
817

Leu His Tyr Ile Ala Thr Asn Gly Glu Ser Ala Val Val Gln Leu Pro  
260 265 270

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865

Lys Asn Gly Pro Ile Tyr Asp Val Val Trp Asn Ser Ser Ser Thr Glu  
275 280 285

ttt tgt gct gta tat ggt ttt atg cct gcc aaa gcg aca att ttc aac  
913

Phe Cys Ala Val Tyr Gly Phe Met Pro Ala Lys Ala Thr Ile Phe Asn  
290 295 300

ttg aaa tgt gat cct gta ttt gac ttt gga act ggt cct cgt aat gca  
961

Leu Lys Cys Asp Pro Val Phe Asp Phe Gly Thr Gly Pro Arg Asn Ala  
305 310 315

gcc tac tat agc cct cat gga cat ata tta gta tta gct gga ttt gga  
1009

Ala Tyr Tyr Ser Pro His Gly His Ile Leu Val Leu Ala Gly Phe Gly  
320 325 330 335

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1057

Asn Leu Arg Gly Gln Met Glu Val Trp Asp Val Lys Asn Tyr Lys Leu  
340 345 350

att tct aaa ccg gtg gct tct gat tct aca tat ttt gct tgg tgc ccg  
1105

Ile Ser Lys Pro Val Ala Ser Asp Ser Thr Tyr Phe Ala Trp Cys Pro  
355 360 365

gat ggt gag cat att tta aca gct aca tgt gct ccc agg tta cgg gtt  
1153

Asp Gly Glu His Ile Leu Thr Ala Thr Cys Ala Pro Arg Leu Arg Val  
370 375 380

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T05T90 25 FEB 60

aat aat gga tac aaa att tgg cat tat act ggc tct atc ttg cac aag  
1201  
Asn Asn Gly Tyr Lys Ile Trp His Tyr Thr Gly Ser Ile Leu His Lys  
385 390 395

tat gat gtg cca tca aat gca gaa tta tgg cag gtt tct tgg cag cca  
1249  
Tyr Asp Val Pro Ser Asn Ala Glu Leu Trp Gln Val Ser Trp Gln Pro  
400 405 410 415

ttt ttg gat gga ata ttt cca gca aaa aca ata act tac caa gca gtt  
1297  
Phe Leu Asp Gly Ile Phe Pro Ala Lys Thr Ile Thr Tyr Gln Ala Val  
420 425 430

cca agt gaa gta ccc aat gag gaa cct aaa gtt gca aca gct tat aga  
1345  
Pro Ser Glu Val Pro Asn Glu Glu Pro Lys Val Ala Thr Ala Tyr Arg  
435 440 445

ccc cca gct tta aga aat aaa cca atc acc aat tcc aaa ttg cat gaa  
1393  
Pro Pro Ala Leu Arg Asn Lys Pro Ile Thr Asn Ser Lys Leu His Glu  
450 455 460

gag gaa cca cct cag aat atg aaa cca caa tca gga aac gat aag cca  
1441  
Glu Glu Pro Pro Gln Asn Met Lys Pro Gln Ser Gly Asn Asp Lys Pro  
465 470 475

tta tca aaa aca gct ctt aaa aat caa agg aag cat gaa gct aag aaa  
1489  
Leu Ser Lys Thr Ala Leu Lys Asn Gln Arg Lys His Glu Ala Lys Lys  
480 485 490 495

gct gca aag cag gaa gca aga agt gac aag agt cca gat ttg gca cct  
1537  
Ala Ala Lys Gln Glu Ala Arg Ser Asp Lys Ser Pro Asp Leu Ala Pro  
500 505 510

act cct gcc cca cag agc aca cca cga aac act gtc tct cag tca att  
1585  
Thr Pro Ala Pro Gln Ser Thr Pro Arg Asn Thr Val Ser Gln Ser Ile  
515 520 525

tct ggg gac cct gag ata gac aaa aaa atc aag aac cta aag aag aaa  
1633  
Ser Gly Asp Pro Glu Ile Asp Lys Lys Ile Lys Asn Leu Lys Lys Lys  
530 535 540

ctg aaa gca atc gaa caa ctg aaa gaa caa gca gca act gga aaa cag  
1681  
Leu Lys Ala Ile Glu Gln Leu Lys Glu Gln Ala Ala Thr Gly Lys Gln  
545 550 555

cta gaa aaa aat cag ttg gag aaa att cag aaa gaa aca gcc ctt ctc  
1729

Leu Glu Lys Asn Gln Leu Glu Lys Ile Gln Lys Glu Thr Ala Leu Leu  
560 565 570 575

cag gag ctg gaa gat ttg gaa ttg ggt att t aaagattcac ggaaagcaag  
1780

Gln Glu Leu Glu Asp Leu Glu Leu Gly Ile  
580 585

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1840  
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1949

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35 40 45  
Thr Leu Phe Ala Trp Gly Asn Gly Glu Lys Val Asn Ile Ile Ser Val  
50 55 60  
Thr Asn Lys Gly Leu Leu His Ser Phe Asp Leu Leu Lys Ala Val Cys  
65 70 75 80  
Leu Glu Phe Ser Pro Lys Asn Thr Val Leu Ala Thr Trp Gln Pro Tyr  
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Thr Thr Ser Lys Asp Gly Thr Ala Gly Ile Pro Asn Leu Gln Leu Tyr  
100 105 110  
Asp Val Lys Thr Gly Thr Cys Leu Lys Ser Phe Ile Gln Lys Lys Met  
115 120 125  
Gln Asn Trp Cys Pro Ser Trp Ser Glu Asp Glu Thr Leu Cys Ala Arg  
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Pro Gly Pro Gln Pro Tyr Lys Val Ala Val Tyr Val Pro Gly Ser Lys  
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225 230 235 240  
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245 250 255  
His Tyr Ile Ala Thr Asn Gly Glu Ser Ala Val Val Gln Leu Pro Lys  
260 265 270  
Asn Gly Pro Ile Tyr Asp Val Val Trp Asn Ser Ser Ser Thr Glu Phe  
275 280 285



Cys Ala Val Tyr Gly Phe Met Pro Ala Lys Ala Thr Ile Phe Asn Leu  
 290 295 300  
 Lys Cys Asp Pro Val Phe Asp Phe Gly Thr Gly Pro Arg Asn Ala Ala  
 305 310 315 320  
 Tyr Tyr Ser Pro His Gly His Ile Leu Val Leu Ala Gly Phe Gly Asn  
 325 330 335  
 Leu Arg Gly Gln Met Glu Val Trp Asp Val Lys Asn Tyr Lys Leu Ile  
 340 345 350  
 Ser Lys Pro Val Ala Ser Asp Ser Thr Tyr Phe Ala Trp Cys Pro Asp  
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 Gly Glu His Ile Leu Thr Ala Thr Cys Ala Pro Arg Leu Arg Val Asn  
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 385 390 395 400  
 Asp Val Pro Ser Asn Ala Glu Leu Trp Gln Val Ser Trp Gln Pro Phe  
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 Ser Glu Val Pro Asn Glu Glu Pro Lys Val Ala Thr Ala Tyr Arg Pro  
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 515 520 525  
 Gly Asp Pro Glu Ile Asp Lys Lys Ile Lys Asn Leu Lys Lys Lys Leu  
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 Lys Ala Ile Glu Gln Leu Lys Glu Gln Ala Ala Thr Gly Lys Gln Leu  
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206  
Thr Glu Arg Ile His Leu Arg Asn Pro Ser Ala Ala Phe Phe Cys Val  
30 35 40

254  
Ala Arg Leu Gln Asp Phe Lys Leu Asp Phe Gly Asn Ser Gln Gly Lys  
45 50 55

302  
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60 65 70 75

350  
Gly Asp Glu Val Trp Gly Val Val Trp Lys Met Asn Lys Ser Asn Leu  
80 85 90

398  
Asn Ser Leu Asp Glu Gln Glu Gly Val Lys Ser Gly Met Tyr Val Val  
95 100 105

446  
Ile Glu Val Lys Val Ala Thr Gln Glu Gly Lys Glu Ile Thr Cys Arg  
110 115 120

494  
Ser Tyr Leu Met Thr Asn Tyr Glu Ser Ala Pro Pro Ser Pro Gln Tyr  
125 130 135

542  
Lys Lys Ile Ile Cys Met Gly Ala Lys Glu Asn Gly Leu Pro Leu Glu  
140 145 150 155

590  
Tyr Gln Glu Lys Leu Lys Ala Ile Glu Pro Asn Asp Tyr Thr Gly Lys  
160 165 170

638  
Val Ser Glu Glu Ile Glu Asp Ile Ile Lys Lys Gly Glu Thr Gln Thr  
175 180 185

10



gtagtgggcc ccagtgttgc gctctctggc cgttccttac actttgcttc aggtccagt  
60

gcaggggcgt agtgggat atg gcc aac tcg ggc tgc aag gac gtc acg ggt  
111

Met Ala Asn Ser Gly Cys Lys Asp Val Thr Gly  
1 5 10

cca gat gag gag agt ttt ctg tac ttt gcc tac ggc agc aac ctg ctg  
159

Pro Asp Glu Glu Ser Phe Leu Tyr Phe Ala Tyr Gly Ser Asn Leu Leu  
15 20 25

aca gag agg atc cac ctc cga aac ccc tcg gcg gcg ttc ttc tgt gtg  
207

Thr Glu Arg Ile His Leu Arg Asn Pro Ser Ala Ala Phe Phe Cys Val  
30 35 40

gcc cgc ctg cag gca aga agg ggt t aaaagtggaa tgtatgttgt  
252

Ala Arg Leu Gln Ala Arg Arg Gly  
45 50

aatagaagtt aaagttgcaa ctcaagaagg aaaagaaata acctgtcgaa gttatctgat  
312

gacaaattac gaaagtgctc ccccatcccc acagtataaa aagattattt gcatgggtgc  
372

aaaagaaaat ggtttgccgc tggagtatca agagaagtta aaagcaatag aaccaaata  
432

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492

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552

aacacttgag aacagggatc tgggggatct ccacgtttga tccattttca gcagtgtctt  
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852

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<211> 51

<212> PRT

<213> H. sapiens

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Leu Arg Asn Pro Ser Ala Ala Phe Phe Cys Val Ala Arg Leu Gln Ala  
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Arg Arg Gly  
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 <212> DNA  
 <213> H. sapiens

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 120  
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 gtcaggccac caactatggt gaggacctga cccggcacca cgatgagctg tgagccccgc  
 240  
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 300  
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 360  
 gggctctcag ggacccccctg ggtcggcttc tgtccctgtc acacccccaa cccagggag  
 420  
 gggctgtcat agtcccagag gataagcaat acctatttct gactgagtct cccagcccag  
 480  
 acccaggga cctggcccca agctcagctc taagaaccgc caccaacccc tccagctcca  
 540  
 aatctgagcc tccaccacat agactgaaac tccctggcc ccagccctct cctgctctggc  
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 <223> n = A,T,C or G

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 120  
 cccagacgc aggcctcat ggccagggga ggtgaccca ggcgcccc ctgagcgacg  
 180  
 ctccccatga tgacgccac gggaacttcc agtacgacca tgaggcttcc ctgggacggg  
 240  
 aagtggccaa ggaattcgac caactacccc cagaggaaag ccaggcccgt ctggggcgga  
 300  
 tcgtggaccg catggaccgc gcgggggacg gcgacggctg ggtgtcgctg gccagcttc  
 360

cgcggtggat	cgcgcacacg	cagcagcggc	acatacggga	ctcgggtgagc	gcggccttggg
420					
acacgtacga	cacggaccgc	gacggggcgtg	tgggttggga	ggagctgcmc	aacgccacct
480					
atggccacta	cgcgcccggg	gaagaatttc	atgacgtgga	ggatgcagag	acctacaaaa
540					
agatgctggc	tcgggacgag	cggcggtttcc	gggtggccga	ccaggatggg	gactcgatgg
600					
ccactcgaga	ggagctgaca	gccttcctgc	accccagagga	gttcctcac	atgcggggaca
660					
tcgtgattgc	tgaaaccttg	gaggacctgg	acagaaacaa	agatggctat	gtccagggtgg
720					
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780					
agacggagag	gcagcagttc	cgggacttcc	gggatctgaa	caaggatggg	cacctggatg
840					
ggagtgaagg	gggccactgg	gtgctgcccc	ctgccagga	ccagcccctg	gtggaagcca
900					
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960					
tgggtaattg	gaacatgttt	gtgggcagtc	aggccaccaa	ctatggygag	gacctgacct
1020					
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1080					
accggaggag	gggccgctgt	ggtctggccc	cctccctgtc	caggccccgc	aggaggcaga
1140					
tgcagtccca	ggcatcctcc	tkccctggg	ctctcagga	ccccctgggt	cggcttctgt
1200					
ccctgtcaca	cccccaacct	cagggagggg	ctgtcatagt	cccagaggat	aagcaatacc
1260					
tattttctgac	tgagtctccc	agcccagacc	caggggacct	nggccccaa	ctcagctcta
1320					
agaaccgccc	caaccctccc	agctccaaat	ctgagcctcc	accacataga	ctgaaactcc
1380					
cctggcccca	gccctctcct	gcctggcctg	gcctgggaca	cctcctctct	gccaggaggc
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<210> 13
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<212> DNA
<213> H. sapiens
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111
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cag gtt gca gaa aat cct cac tct gag tac ggt ctc aca gac aac gtt  
159

Gln Val Ala Glu Asn Pro His Ser Glu Tyr Gly Leu Thr Asp Asn Val  
15 20 25

gag aga ata gta gaa aat gag aag att aat gca gaa aag tca tca aag  
207

Glu Arg Ile Val Glu Asn Glu Lys Ile Asn Ala Glu Lys Ser Ser Lys  
30 35 40

cag aag gta gat ctc cag tct ttg cca act cgt gcc tac ctg gat cag  
255

Gln Lys Val Asp Leu Gln Ser Leu Pro Thr Arg Ala Tyr Leu Asp Gln  
45 50 55

aca gtt gtg cct atc tta tta cag gga ctt gct gtg ctt gca aag gaa  
303

Thr Val Val Pro Ile Leu Leu Gln Gly Leu Ala Val Leu Ala Lys Glu  
60 65 70 75

aga cca cca aat ccc att gaa ttt cta gca tct tat ctt tta aaa aac  
351

Arg Pro Pro Asn Pro Ile Glu Phe Leu Ala Ser Tyr Leu Leu Lys Asn  
80 85 90

aag gca cag ttt gaa gat cga aac t gacttaatgg gaagaacaga  
396

Lys Ala Gln Phe Glu Asp Arg Asn  
95

aaaatttagt tgctactgta gatttacatg attaagaggc agctttaatt gccatgatca  
456

ttccctcttt ttggatgtat aagaaccttc cggacaacag aacctatttc tggaattgca  
516

gaagataaca tatttccctt attttgattt aatcaccata aaccatacct atttaatgag  
576

tgtattctgt gcaatttttt tctcagattg tctttaactt tgtttttaaa atgaccttca  
636

aaataaaactg tcaaaacacc attat  
661

<210> 14

<211> 99

<212> PRT

<213> H. sapiens

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Met Glu Pro Glu Gln Met Leu Glu Gly Gln Thr Gln Val Ala Glu Asn  
1 5 10 15

Pro His Ser Glu Tyr Gly Leu Thr Asp Asn Val Glu Arg Ile Val Glu  
20 25 30

Asn Glu Lys Ile Asn Ala Glu Lys Ser Ser Lys Gln Lys Val Asp Leu  
35 40 45

Gln Ser Leu Pro Thr Arg Ala Tyr Leu Asp Gln Thr Val Val Pro Ile  
50 55 60

Leu Leu Gln Gly Leu Ala Val Leu Ala Lys Glu Arg Pro Pro Asn Pro

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<222> 1047, 1301  
<223> n = A,T,C or G
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16



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 tatttctgac tgagtctccc agcccagacc cagggaccct nggccccaaag ctcagctcta  
 1320  
 agaaccgccc caaccctcc agctccaaat ctgagcctcc accacataga ctgaaactcc  
 1380  
 cctggcccca gccctctcct gcctggcctg gcctgggaca cctcctctct gccaggagggc  
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 aataaaagcc agcgccggga aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa  
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<210> 16  
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 <213> H. sapiens

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 51

Met Ala Asp Val Leu Asp Leu His Glu Ala Gly Gly  
 1 5 10

gaa gat ttc gcc atg gat gag gat ggg gac gag agc att cac aaa ctg  
 99

Glu Asp Phe Ala Met Asp Glu Asp Gly Asp Glu Ser Ile His Lys Leu  
 15 20 25

aaa gaa aaa gcg aag aaa cgg aag ggt cgc ggc ttt ggc tcc gaa gag  
 147

Lys Glu Lys Ala Lys Lys Arg Lys Gly Arg Gly Phe Gly Ser Glu Glu  
 30 35 40

ggg tcc cga gcg cgg atg cgt gag gat tat gac agc gtg gag cag gat  
 195

Gly Ser Arg Ala Arg Met Arg Glu Asp Tyr Asp Ser Val Glu Gln Asp  
 45 50 55 60

ggc gat gaa ccc gga cca caa cgc tct gtt gaa ggc tgg att ctc ttt  
 243

Gly Asp Glu Pro Gly Pro Gln Arg Ser Val Glu Gly Trp Ile Leu Phe  
 65 70 75

gta act gga gtc cat gag gaa gcc acc gaa gaa gac ata cac gac aaa  
 291

Val Thr Gly Val His Glu Glu Ala Thr Glu Glu Asp Ile His Asp Lys  
 80 85 90

ttc gca gaa tat ggg gaa att aaa aac att cat ctc aac ctc gac agg  
 339

Phe Ala Glu Tyr Gly Glu Ile Lys Asn Ile His Leu Asn Leu Asp Arg  
 95 100 105

cga aca gga tat ctg aag ggg tat act cta gtt gaa tat gaa aca tac  
387

Arg Thr Gly Tyr Leu Lys Gly Tyr Thr Leu Val Glu Tyr Glu Thr Tyr  
110 115 120

aag gaa gcc cag gct gct atg gag gga ctc aat ggc cag gat ttg atg  
435

Lys Glu Ala Gln Ala Ala Met Glu Gly Leu Asn Gly Gln Asp Leu Met  
125 130 135 140

gga cag ccc atc agc gtt gac tgg tgt ttt gtt cgg ggt cca cca aaa  
483

Gly Gln Pro Ile Ser Val Asp Trp Cys Phe Val Arg Gly Pro Pro Lys  
145 150 155

ggc aag agg aga ggt ggc cga aga cgc agc aga agt cca gac cgg aga  
531

Gly Lys Arg Arg Gly Gly Arg Arg Arg Ser Arg Ser Pro Asp Arg Arg  
160 165 170

cgt cgc t gacaggtcct ctgttggtcca ggtgttctct tcaagattcc atttgaccat  
588

Arg Arg

gcagccttgg acaaatagga ctgggggtgga acttgctgtg tttatatatta atctcttacc  
648

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716

<210> 17

<211> 174

<212> PRT

<213> H. sapiens

<400> 17

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20 25 30

Lys Lys Arg Lys Gly Arg Gly Phe Gly Ser Glu Glu Gly Ser Arg Ala  
35 40 45

Arg Met Arg Glu Asp Tyr Asp Ser Val Glu Gln Asp Gly Asp Glu Pro  
50 55 60

Gly Pro Gln Arg Ser Val Glu Gly Trp Ile Leu Phe Val Thr Gly Val  
65 70 75 80

His Glu Glu Ala Thr Glu Glu Asp Ile His Asp Lys Phe Ala Glu Tyr  
85 90 95

Gly Glu Ile Lys Asn Ile His Leu Asn Leu Asp Arg Arg Thr Gly Tyr  
100 105 110

Leu Lys Gly Tyr Thr Leu Val Glu Tyr Glu Thr Tyr Lys Glu Ala Gln  
115 120 125

Ala Ala Met Glu Gly Leu Asn Gly Gln Asp Leu Met Gly Gln Pro Ile  
130 135 140

Ser Val Asp Trp Cys Phe Val Arg Gly Pro Pro Lys Gly Lys Arg Arg  
 145 150 155 160  
 Gly Gly Arg Arg Arg Ser Arg Ser Pro Asp Arg Arg Arg Arg  
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Met Ala Lys Pro Cys Gly Val Arg Leu Ser Gly Glu Ala Arg Lys Gln  
 1 5 10 15

gtg gag gtc ttc aga cag aat ctt ttc cag gag gct gag gaa ttc ctc  
 97  
 Val Glu Val Phe Arg Gln Asn Leu Phe Gln Glu Ala Glu Glu Phe Leu  
 20 25 30

tac aga ttc ttg cca cag aaa atc ata tac ctg aat cag ctc ttg caa  
 145  
 Tyr Arg Phe Leu Pro Gln Lys Ile Ile Tyr Leu Asn Gln Leu Leu Gln  
 35 40 45

gag gac tcc ctc aat gtg gct gac ttg act tcc ctc cgg gcc cca ctg  
 193  
 Glu Asp Ser Leu Asn Val Ala Asp Leu Thr Ser Leu Arg Ala Pro Leu  
 50 55 60

gac atc ccc atc cca gac cct cca ccc aag gat gat gag atg gaa aca  
 241  
 Asp Ile Pro Ile Pro Asp Pro Pro Pro Lys Asp Asp Glu Met Glu Thr  
 65 70 75 80

gat aag cag gag aag aaa gaa gtc cct aag tgt gga ttt ctc cct ggg  
 289  
 Asp Lys Gln Glu Lys Lys Glu Val Pro Lys Cys Gly Phe Leu Pro Gly  
 85 90 95

aat gag aaa gtc ctg tcc ctg ctt gcc ctg gtt aag cca gaa gtc tgg  
 337  
 Asn Glu Lys Val Leu Ser Leu Leu Ala Leu Val Lys Pro Glu Val Trp  
 100 105 110

act ctc aaa gag aaa tgc att ctg gtg att aca tgg atc caa cac ctg  
 385  
 Thr Leu Lys Glu Lys Cys Ile Leu Val Ile Thr Trp Ile Gln His Leu  
 115 120 125

atc ccc aag att gaa gat gga aat gat ttt ggg gta gca atc cag gag  
 433  
 Ile Pro Lys Ile Glu Asp Gly Asn Asp Phe Gly Val Ala Ile Gln Glu

130

135

140

aag gtg ctg gag agg gtg aat gcc gtc aag acc aaa gtg aag ctt tcc  
481

481  
Lys Val Leu Glu Arg Val Asn Ala Val Lys Thr Lys Val Lys Leu Ser  
145 150 155 160

aga caa cca ttt cca agt act tct cag aac gtg ggg atg ctg tgg cca  
529

Arg Gln Pro Phe Pro Ser Thr Ser Gln Asn Val Gly Met Leu Trp Pro  
165 170 175

agg cct cca agg aga ctc atg t aatggattac cgggccttg tgcatgagcg  
581

Arg Pro Pro Arg Arg Leu Met  
180

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641

641  
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<210> 19

<211> 183

<212> PRT

<213> H. sapiens

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Tyr Arg Phe Leu Pro Gln Lys Ile Tyr Leu Asn Gln Leu Leu Gln

Glu Asp Ser Leu Asn Val Ala Asp Leu Thr Ser Leu Arg Ala Pro Leu

Asp Ile Pro Ile Pro Asp Pro Pro Lys Asp Asp Glu Met Glu Thr  
65 70 75 80

Asp Lys Gln Glu Lys Lys Glu Val Pro Lys Cys Gly Phe Leu Pro Gly

Asn Glu Lys Val Leu Ser Leu Leu Ala Leu Val Lys Pro Glu Val Trp  
100 105 110

Thr Leu Lys Glu Lys Cys Ile Leu Val Ile Thr Trp Ile Gln His Leu

Ile Pro Lys Ile Glu Asp Gly Asn Asp Phe Gly Val Ala Ile Gln Glu

Lys Val Leu Glu Arg Val Asn Ala Val Lys Thr Lys Val Lys Leu Ser  
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Arg Gln Pro Phe Pro Ser Thr Ser Gln Asn Val Gly Met Leu Trp Pro

Arg Pro Pro Arg Arg Leu Met  
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 239  
 atg ttt tcc ata cga atc ctc tct tct tca gct ttt tgt tct tgt tcc  
 287  
 Met Phe Ser Ile Arg Ile Leu Ser Ser Ser Ala Phe Cys Ser Cys Ser  
 1 5 10 15  
 ttc ctg gcc tgc tct tca gct ctt tct ttt tta att ttt tcc agt tct  
 335  
 Phe Leu Ala Cys Ser Ser Ala Leu Ser Phe Leu Ile Phe Ser Ser Ser  
 20 25 30  
 gca aga aga gct gca gta tca tca tca tca ctt tct tct tca aaa tct  
 383  
 Ala Arg Arg Ala Ala Val Ser Ser Ser Ser Leu Ser Ser Ser Lys Ser  
 35 40 45  
 tca tct tcc tca tct gtt aga ggg tca tct gca tca agg ttg gcg gca  
 431  
 Ser Ser Ser Ser Ser Val Arg Gly Ser Ser Ala Ser Arg Leu Ala Ala  
 50 55 60  
 gga atc tgg tct aac cgt ggc ttt ttt gac act gaa gag gag gtt gta  
 479  
 Gly Ile Trp Ser Asn Arg Gly Phe Phe Asp Thr Glu Glu Glu Val Val  
 65 70 75 80  
 tgt tct cgg gtt gga cga tcc cta ttt ttc tct ctt gca gca gct ctc  
 527  
 Cys Ser Arg Val Gly Arg Ser Leu Phe Phe Ser Leu Ala Ala Ala Leu  
 85 90 95  
 tct ctt tct tcc aac tct ctc ctg aag tca cgg tta cga acc tct tca  
 575  
 Ser Leu Ser Ser Asn Ser Leu Leu Lys Ser Arg Leu Arg Thr Ser Ser  
 100 105 110  
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 625  
 Gly Ala Ser  
 115

09883152.061501

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Phe Leu Ala Cys Ser Ser Ala Leu Ser Phe Leu Ile Phe Ser Ser Ser  
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Ala Arg Arg Ala Ala Val Ser Ser Ser Leu Ser Ser Ser Lys Ser  
35 40 45  
Ser Ser Ser Ser Ser Val Arg Gly Ser Ser Ala Ser Arg Leu Ala Ala  
50 55 60  
Gly Ile Trp Ser Asn Arg Gly Phe Phe Asp Thr Glu Glu Glu Val Val  
65 70 75 80  
Cys Ser Arg Val Gly Arg Ser Leu Phe Phe Ser Leu Ala Ala Ala Leu  
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Ser Leu Ser Ser Asn Ser Leu Leu Lys Ser Arg Leu Arg Thr Ser Ser  
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Gly Ala Ser  
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<222> (53)...(1700)

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58

Met Lys  
1

agg cct aag tta aag aaa gca agt aaa cgc atg acc tgc cat aag cgg  
106  
Arg Pro Lys Leu Lys Lys Ala Ser Lys Arg Met Thr Cys His Lys Arg  
5 10 15

tat aaa atc caa aaa aag gtt cga gaa cat cat cga aaa tta aga aag  
154  
Tyr Lys Ile Gln Lys Lys Val Arg Glu His His Arg Lys Leu Arg Lys  
20 25 30

gag gct aaa aag cag ggt cac aag aag cct agg aaa gac cca gga gtt  
202  
Glu Ala Lys Lys Gln Gly His Lys Lys Pro Arg Lys Asp Pro Gly Val

35	40										45										50									
cca aac agt gct ccc ttt aag gag gct ctt ctt agg gaa gct gag cta																														
250																														
Pro Asn Ser Ala Pro Phe Lys Glu Ala Leu Leu Arg Glu Ala Glu Leu																														
	55										60										65									
agg aaa cag agg ctt gaa gaa cta aaa cag cag cag aaa ctt gac agg																														
298																														
Arg Lys Gln Arg Leu Glu Glu Leu Lys Gln Gln Gln Lys Leu Asp Arg																														
	70										75										80									
cag aag gaa cta gaa aag aaa aga aaa ctt gaa act aat cct gat att																														
346																														
Gln Lys Glu Leu Glu Lys Lys Arg Lys Leu Glu Thr Asn Pro Asp Ile																														
	85										90										95									
aag cca tca aat gtg gaa cct atg gaa aag gag ttt ggg ctt tgc aaa																														
394																														
Lys Pro Ser Asn Val Glu Pro Met Glu Lys Glu Phe Gly Leu Cys Lys																														
	100										105										110									
act gag aac aaa gcc aag tcg ggc aaa cag aat tca aag aag ctg tac																														
442																														
Thr Glu Asn Lys Ala Lys Ser Gly Lys Gln Asn Ser Lys Lys Leu Tyr																														
115	120										125										130									
tgc caa gaa ctt aaa aag gtg att gaa gcc tcc gat gtt gtc cta gag																														
490																														
Cys Gln Glu Leu Lys Lys Val Ile Glu Ala Ser Asp Val Val Leu Glu																														
	135										140										145									
gtg ttg gat gcc aga gat cct ctt ggt tgc aga tgt cct cag gta gaa																														
538																														
Val Leu Asp Ala Arg Asp Pro Leu Gly Cys Arg Cys Pro Gln Val Glu																														
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gag gcc att gtc cag agt gga cag aaa aag ctg gta ctt ata tta aat																														
586																														
Glu Ala Ile Val Gln Ser Gly Gln Lys Lys Leu Val Leu Ile Leu Asn																														
	165										170										175									
aaa tca gat ctg gta cca aag gag aat ttg gag agc tgg cta aat tat																														
634																														
Lys Ser Asp Leu Val Pro Lys Glu Asn Leu Glu Ser Trp Leu Asn Tyr																														
	180										185										190									
ttg aag aaa gaa ttg cca aca gtg gtg ttc aga gcc tca aca aaa cca																														
682																														
Leu Lys Lys Glu Leu Pro Thr Val Val Phe Arg Ala Ser Thr Lys Pro																														
195	200										205										210									
aag gat aaa ggg aag ata acc aag cgt gtg aag gca aag aag aat gct																														
730																														
Lys Asp Lys Gly Lys Ile Thr Lys Arg Val Lys Ala Lys Lys Asn Ala																														
	215										220										225									

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778  
Ala Pro Phe Arg Ser Glu Val Cys Phe Gly Lys Glu Gly Leu Trp Lys  
230 235 240

ctt ctt gga ggt ttt cag gaa act tgc agc aaa gcc att cgg gtt gga  
826  
Leu Leu Gly Gly Phe Gln Glu Thr Cys Ser Lys Ala Ile Arg Val Gly  
245 250 255

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874  
Val Ile Gly Phe Pro Asn Val Gly Lys Ser Ser Ile Ile Asn Ser Leu  
260 265 270

aaa caa gaa cag atg tgt aat gtt ggt gta tcc atg ggg ctt aca agg  
922  
Lys Gln Glu Gln Met Cys Asn Val Gly Val Ser Met Gly Leu Thr Arg  
275 280 285 290

agc atg caa gtt gtc ccc ttg gac aaa cag atc aca atc ata gat agt  
970  
Ser Met Gln Val Val Pro Leu Asp Lys Gln Ile Thr Ile Ile Asp Ser  
295 300 305

ccg agc ttc atc gta tct cca ctt aat tcc tcc tct gcg ctt gct ctg  
1018  
Pro Ser Phe Ile Val Ser Pro Leu Asn Ser Ser Ser Ala Leu Ala Leu  
310 315 320

cga agt cca gca agt att gaa gta gta aaa ccg atg gag gct gcc agt  
1066  
Arg Ser Pro Ala Ser Ile Glu Val Val Lys Pro Met Glu Ala Ala Ser  
325 330 335

gcc atc ctt tcc cag gct gat gct cga cag gta gta ctg aaa tat act  
1114  
Ala Ile Leu Ser Gln Ala Asp Ala Arg Gln Val Val Leu Lys Tyr Thr  
340 345 350

gtc cca ggc tac agg aat tct ctg gaa ttt ttt act atg ctt gct cag  
1162  
Val Pro Gly Tyr Arg Asn Ser Leu Glu Phe Phe Thr Met Leu Ala Gln  
355 360 365 370

aga aga ggt atg cac caa aaa ggt gga atc cca aat gtt gaa ggt gct  
1210  
Arg Arg Gly Met His Gln Lys Gly Gly Ile Pro Asn Val Glu Gly Ala  
375 380 385

gcc aaa ctg ctg tgg tct gag tgg aca ggt gcc tca tta gct tac tat  
1258  
Ala Lys Leu Leu Trp Ser Glu Trp Thr Gly Ala Ser Leu Ala Tyr Tyr  
390 395 400

tgc cat ccc cct aca tct tgg act cct cct cca tat ttt aat gag agt  
1306





[illegible]

Met	Lys	Arg	Pro	Lys	Leu	Lys	Lys	Ala	Ser	Lys	Arg	Met	Thr	Cys	His
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Lys	Arg	Tyr	Lys	Ile	Gln	Lys	Lys	Val	Arg	Glu	His	His	Arg	Lys	Leu
			20					25					30		
Arg	Lys	Glu	Ala	Lys	Lys	Gln	Gly	His	Lys	Lys	Pro	Arg	Lys	Asp	Pro
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Gly	Val	Pro	Asn	Ser	Ala	Pro	Phe	Lys	Glu	Ala	Leu	Leu	Arg	Glu	Ala
	50					55					60				
Glu	Leu	Arg	Lys	Gln	Arg	Leu	Glu	Glu	Leu	Lys	Gln	Gln	Gln	Lys	Leu
65				70						75					80
Asp	Arg	Gln	Lys	Glu	Leu	Glu	Lys	Lys	Arg	Lys	Leu	Glu	Thr	Asn	Pro
				85					90					95	
Asp	Ile	Lys	Pro	Ser	Asn	Val	Glu	Pro	Met	Glu	Lys	Glu	Phe	Gly	Leu
			100						105					110	
Cys	Lys	Thr	Glu	Asn	Lys	Ala	Lys	Ser	Gly	Lys	Gln	Asn	Ser	Lys	Lys
		115					120					125			
Leu	Tyr	Cys	Gln	Glu	Leu	Lys	Lys	Val	Ile	Glu	Ala	Ser	Asp	Val	Val
	130					135						140			
Leu	Glu	Val	Leu	Asp	Ala	Arg	Asp	Pro	Leu	Gly	Cys	Arg	Cys	Pro	Gln
145				150						155					160
Val	Glu	Glu	Ala	Ile	Val	Gln	Ser	Gly	Gln	Lys	Lys	Leu	Val	Leu	Ile
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Asn	Tyr	Leu	Lys	Lys	Glu	Leu	Pro	Thr	Val	Val	Phe	Arg	Ala	Ser	Thr
		195					200					205			
Lys	Pro	Lys	Asp	Lys	Gly	Lys	Ile	Thr	Lys	Arg	Val	Lys	Ala	Lys	Lys
	210					215					220				
Asn	Ala	Ala	Pro	Phe	Arg	Ser	Glu	Val	Cys	Phe	Gly	Lys	Glu	Gly	Leu
225				230						235					240
Trp	Lys	Leu	Leu	Gly	Gly	Phe	Gln	Glu	Thr	Cys	Ser	Lys	Ala	Ile	Arg
				245						250				255	
Val	Gly	Val	Ile	Gly	Phe	Pro	Asn	Val	Gly	Lys	Ser	Ser	Ile	Ile	Asn
			260						265					270	
Ser	Leu	Lys	Gln	Glu	Gln	Met	Cys	Asn	Val	Gly	Val	Ser	Met	Gly	Leu
		275					280					285			
Thr	Arg	Ser	Met	Gln	Val	Val	Pro	Leu	Asp	Lys	Gln	Ile	Thr	Ile	Ile
	290					295					300				
Asp	Ser	Pro	Ser	Phe	Ile	Val	Ser	Pro	Leu	Asn	Ser	Ser	Ser	Ala	Leu
305				310						315					320
Ala	Leu	Arg	Ser	Pro	Ala	Ser	Ile	Glu	Val	Val	Lys	Pro	Met	Glu	Ala
				325						330				335	
Ala	Ser	Ala	Ile	Leu	Ser	Gln	Ala	Asp	Ala	Arg	Gln	Val	Val	Leu	Lys
			340						345					350	
Tyr	Thr	Val	Pro	Gly	Tyr	Arg	Asn	S							

00000152.061501

405 410 415  
 Glu Ser Ile Val Val Asp Met Lys Ser Gly Phe Asn Leu Glu Glu Leu  
 420 425 430  
 Glu Lys Asn Asn Ala Gln Ser Ile Arg Ala Ile Lys Gly Pro His Leu  
 435 440 445  
 Ala Asn Ser Ile Leu Phe Gln Ser Ser Gly Leu Thr Asn Gly Ile Ile  
 450 455 460  
 Glu Glu Lys Asp Ile His Glu Glu Leu Pro Lys Arg Lys Glu Arg Lys  
 465 470 475 480  
 Gln Glu Glu Arg Glu Asp Asp Lys Asp Ser Asp Gln Glu Thr Val Asp  
 485 490 495  
 Glu Glu Val Asp Glu Asn Ser Ser Gly Met Phe Ala Ala Glu Glu Thr  
 500 505 510  
 Gly Glu Ala Leu Ser Glu Glu Thr Thr Ala Gly Glu Gln Ser Thr Arg  
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 ggg aag gtg att ggg aca aaa atg caa aag act gct aaa gtg aga gtg  
 99  
 Gly Lys Val Ile Gly Thr Lys Met Gln Lys Thr Ala Lys Val Arg Val  
 15 20 25 30  
  
 acc agg ctt gtt ctg gat ccc tat tta tta aag tat ttt aat aag cgg  
 147  
 Thr Arg Leu Val Leu Asp Pro Tyr Leu Leu Lys Tyr Phe Asn Lys Arg  
 35 40 45  
  
 aaa acc tac ttt gct cac gat gcc ctt cag cag tgc aca gtt ggg gat  
 195  
 Lys Thr Tyr Phe Ala His Asp Ala Leu Gln Gln Cys Thr Val Gly Asp  
 50 55 60  
  
 att gtg ctt ctc aga gct tta cct gtt cca cga gca aag cat gtg aaa  
 243  
 Ile Val Leu Leu Arg Ala Leu Pro Val Pro Arg Ala Lys His Val Lys  
 65 70 75  
  
 cat gaa ctg gct gag atc gtt ttc aaa gtt gga aaa gtc ata gat cca  
 291  
 His Glu Leu Ala Glu Ile Val Phe Lys Val Gly Lys Val Ile Asp Pro

90

Val	Thr	Gly	Lys	Pro	Cys	Ala	Gly	Thr	Thr	Tyr	Leu	Glu	Ser	Pro	Leu
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115 120 125

Ser Ser Ala Gln  
130

503

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Ala Gln  
130

<213> H. sapiens

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180  
gttgaaatgg tggagtccaa cttgcctgga ccagcttaat ggttctgctc ctggtaacgt  
240  
ttttatccat ggatgacttg cttgggtaag gacatgaaga cagttcctgt catacctttt  
300  
aaaggatatg agagtcgggt tgactacact gtgtggagca agttttaaag aagcaaagga  
360  
ctcagaattc atgattgaag aaatgcaggc agacctgtta tcctaaacta gggtttttaa  
420  
tgaccacaac aagcaagcat gcagcttact gcttgaaagg gtcttgctc acccaagcta  
480  
gagtgcagtg gcctttgaag cttactacag cctcaaactt ctgggctcaa gtgatcctca  
540  
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120  
gaagttgaaa tgggtggagtc caacttgcct ggaccagctt aatggttctg ctcttggtaa  
180  
cgtttttata catggatgac ttgcttgggt atggagagtc ggcttgacta cactgtgtgg  
240  
agcaagtttt aaagaagcaa aggactcaga attcatgatt gaagaaatgc aggcagacct  
300  
gttatcctaa actaggggttt tta atg acc aca aca agc aag cat gca gct tac  
353

Met Thr Thr Thr Ser Lys His Ala Ala Tyr  
1 5 10

tgc ttg aaa ggg tct tgc ctc acc caa gct aga gtg cag tgg cct ttg  
401  
Cys Leu Lys Gly Ser Cys Leu Thr Gln Ala Arg Val Gln Trp Pro Leu  
15 20 25

aag ctt act aca gcc tca aac ttc tgg gct caa gtg atc ctc agc ctc  
449  
Lys Leu Thr Thr Ala Ser Asn Phe Trp Ala Gln Val Ile Leu Ser Leu  
30 35 40

cca gtg gtc ttt gta gac tgc ctg atg gag tct cat ggc aca aga aga  
497  
Pro Val Val Phe Val Asp Cys Leu Met Glu Ser His Gly Thr Arg Arg

45

50

55

tta aaa cag tgt ctc caa ttt t aataaatttt tgcaatccaa aaaaaaaaaa  
549

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559

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<213> H. sapiens

<400> 28

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Leu	Thr	Gln	Ala	Arg	Val	Gln	Trp	Pro	Leu	Lys	Leu	Thr	Thr	Ala	Ser
		20					25					30			
Asn	Phe	Trp	Ala	Gln	Val	Ile	Leu	Ser	Leu	Pro	Val	Val	Phe	Val	Asp
	35					40					45				
Cys	Leu	Met	Glu	Ser	His	Gly	Thr	Arg	Arg	Leu	Lys	Gln	Cys	Leu	Gln
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Phe

65

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<213> H. sapiens

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120  
actgaagtcc taaagagcaa gcctaactca agccattggc acacagggcat tagacagaaa  
180  
gctggaagtt gaaatggtgg agtccaactt gcctggacca gcttaatggt tctgctcctg  
240  
gtaacgtttt tatccatgga tgacttgctt gggatatggag agtcggcttg actacactgt  
300  
gtggagcaag ttttaaagaa gcaaaggact cagaattcat gattgaagaa atgcaggcag  
360  
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420  
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480  
tcaaacttct gggctcaagt gatcctcagc ctcccagtgg tctttgtaga ctgcctgatg  
540  
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09283152-061501

caaaaaaaaaa aaaaaaaaaa aaa  
623

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[illegible]

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<210> 67  
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<210> 69  
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<210> 115  
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